

Evan Correa

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EDUCATION

New Jersey Institute of Technology

Newark, NJ

Bachelor of Science in Biology, Dual Minor in Applied Statistics and Mathematics

Sep. 2022 – May 2026

- **Relevant Coursework:** Programming for Bioinformatics, Differential Equations, Calculus III, Linear Algebra, Molecular Biology, Statistical Methods in Data Science, Mathematical Biology, Introduction to Machine Learning (MITx)

RESEARCH EXPERIENCE

Undergraduate Researcher

June 2024 – Present

University of Pennsylvania - Barash Lab

Philadelphia, PA

- Conducted summer research investigation on the regulatory role of RNA-binding proteins in alternative splicing of mRNA and discovered a regulatory interaction between the IGF2BP protein family and the DLEU1 lncRNA.
- Processed RNA-seq data on a high-performance computing (HPC) cluster, assessing quality with FastQC, trimming with BBduk, and aligning reads using STAR, followed by alternative splicing quantification with MAJIQ.
- Published abstract and presented poster to **200+** students and graduate school faculty in a national symposium.
- Continued collaboration remotely with the lab after the summer, focusing on the development of a large-language model (LLM) to predict neuron-specific changes in alternative polyadenylation related to Alzheimer's disease.

Undergraduate Researcher

Jan 2023 – Present

New Jersey Institute of Technology - Severi Lab

Newark, NJ

- Designed and conducted behavioral experiments using optogenetics to modulate neuron activity in live zebrafish to investigate the role of DMRT3a-associated spinal interneurons.
- Bred and maintained a Gal4:UAS transgenic line with the YFP reporter protein and used fluorescent microscopy to identify positive offspring with gene-specific brain and spinal-cord expression patterns.
- Recipient of **\$3,000 research grant** to conduct and present research results at university-wide symposium.

Fellow

Jul 2024 – Sep 2024

Diversity Action Plan for Penn Genomics

Philadelphia, PA

- Participated in NIH-funded program to develop young genomics scientists from underrepresented backgrounds.
- Attended weekly virtual seminars held by the National Human Genome Research Institute.
- Underwent a 2-day intensive R programming workshop to analyze single-cell RNA sequencing data.
- Used primary component analysis (PCA) in combination with Seurat to cluster raw sequencing data based on cell type and gene expression.

Undergraduate Researcher

Sep 2020 – Jan 2023

New Jersey Institute of Technology - Guvendiren Lab

Newark, NJ

- Contributed to a research project focused on developing innovative tissue scaffolds for 3D bioprinting applications.
- Analyzed the morphology of 3D-printed cardiomyocytes cultured on PDMS substrates with varied surface patterns to evaluate cellular responses.
- Co-authored a peer-reviewed research article published in *Advanced Healthcare Materials*.

PRESENTATIONS

1. **Correa, E.**, Severi, K. "Investigating the Effect of Optogenetically Activating Dmrt3a in Larval Zebrafish" *Provost URI Symposium* 2023.
2. **Correa, E.**, Gazzara, M., Barash, Y. "Integrative transcriptomic analysis to characterize RBPs involved in 3' UTR alternative splicing" *Leadership Alliance National Symposium* 2024.
3. **Correa, E.**, Gazzara, M., Barash, Y. "Integrative transcriptomic analysis to characterize RBPs involved in 3' UTR alternative splicing" *Penn SUIP Symposium* 2024.

PUBLICATIONS

1. House, A., Santillan, A., **Correa, E.**, Youssef, V., Guvendiren, M. "Cellular Alignment and Matrix Stiffening Induced Changes in Human Induced Pluripotent Stem Cell Derived Cardiomyocytes" *Advanced Healthcare Materials*, 2024.

HONORS & AWARDS

Full-Ride Merit Award, Albert Dorman Honors College

Provost URI Fellowship, Office of the Provost, New Jersey Institute of Technology

Travel Award, ABRCMS (Annual Biomedical Research Conference for Minoritized Scientists)

Dean's List, New Jersey Institute of Technology

PROGRAMMING PROJECTS

Predicting Diabetes Progression | *Python*

- Leveraged scikit-learn on a synthetic dataset to train a linear regression model for predicting diabetes progression.
- Utilized NumPy, pandas, matplotlib, and Seaborn to construct and interpret a feature correlation matrix.
- Identified triglyceride level, BMI, and serum cholesterol as key features for disease progression.

GenParse | *Python*

- Developed a suite of bioinformatics tools including a FASTA file parser, a function to calculate GC-content, mutation analysis, and basic sequence alignment.
- Implemented a user interface with Tkinter to upload files from local machine and run a user-selected analysis.

TECHNICAL SKILLS

Programming Languages: Python, R, Bash, Java, MATLAB

Libraries: scikit-learn, PyTorch, TensorFlow, pandas, NumPy, matplotlib, Seaborn, Seurat

Software/Tools: Git, ImageJ, Jupyter Notebook, Google Colab, SSH, HPC

Techniques: NGS Analysis, Sequence Alignment, Alternative Splicing Quantification